

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/548, 748  
Source: PCT  
Date Processed by STIC: 09/23 / 2005

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 09/23/2005

PATENT APPLICATION: US/10/548,748

TIME: 14:52:53

Input Set : A:\Sequence listing - 12810-00137-US.txt

Output Set: N:\CRF4\09232005\J548748.raw

3 <110> APPLICANT: Frank, Markus  
 4 Kogel, Karl-Heinz  
 5 Hueckelhoven, Ralph  
 7 <120> TITLE OF INVENTION: METHOD FOR INCREASING RESISTANCE AGAINST STRESS FACTORS IN  
 PLANTS  
 9 <130> FILE REFERENCE: 12810-00137-US  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/548,748  
 C--> 11 <141> CURRENT FILING DATE: 2005-09-08  
 11 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/002436  
 12 <151> PRIOR FILING DATE: 2004-03-10  
 14 <150> PRIOR APPLICATION NUMBER: DE 103 11 118.2  
 15 <151> PRIOR FILING DATE: 2003-03-12  
 17 <160> NUMBER OF SEQ ID NOS: 63  
 19 <170> SOFTWARE: PatentIn version 3.3  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 744  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Hordeum vulgare  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (1)..(741)  
 29 <223> OTHER INFORMATION: coding for BII-protein  
 31 <400> SEQUENCE: 1  
 32 atg gac gcc ttc tac tcg acc tcg tcg gcg gcg gcg agc ggc tgg ggc 48  
 33 Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ser Gly Trp Gly  
 34 1 5 10 15  
 36 cac gac tcc ctc aag aac ttc cgc cag atc tcc ccc gcc gtg cag tcc 96  
 37 His Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val Gln Ser  
 38 20 25 30  
 40 cac ctc aag ctc gtt tac ctg act cta tgc ttt gca ctg gcc tca tct 144  
 41 His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser  
 42 35 40 45  
 44 gcc gtg ggt gct tac cta cac att gcc ctg aac atc ggc ggg atg ctg 192  
 45 Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu  
 46 50 55 60  
 48 aca atg ctc gct tgt gtc gga act atc gcc tgg atg ttc tcg gtg cca 240  
 49 Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro  
 50 65 70 75 80  
 52 gtc tat gag gag agg aag agg ttt ggg ctg ctg atg ggt gca gcc ctc 288  
 53 Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu  
 54 85 90 95  
 56 ctg gaa ggg gct tcg gtt gga cct ctg att gag ctt gcc ata gac ttt 336  
 57 Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe  
 58 100 105 110

Cp9-6)

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60 gac cca agc atc ctc gtg aca ggg ttt gtc gga acc gcc atc gcc ttt 384
61 Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
62      115      120      125
64 ggg tgc ttc tct ggc gcc gcc atc atc gcc aag cgc agg gag tac ctg 432
65 Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu
66      130      135      140
68 tac ctc ggt ggc ctg ctc tcg tct ggc ctg tcg atc ctg ctc tgg ctg 480
69 Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
70 145      150      155      160
72 cag ttt gtc acg tcc atc ttt ggc cac tcc tct ggc agc ttc atg ttt 528
73 Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
74      165      170      175
76 gag gtt tac ttt ggc ctg ttg atc ttc ctg ggg tac atg gtg tac gac 576
77 Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
78      180      185      190
80 acg cag gag atc atc gag agg gcg cac cat ggc gac atg gac tac atc 624
81 Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
82      195      200      205
84 aag cac gcc ctc acc ctc ttc acc gac ttt gtt gcc gtc ctc gtc cga 672
85 Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
86      210      215      220
88 gtc ctc atc atc atg ctc aag aac gca ggc gac aag tcg gag gac aag 720
89 Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
90 225      230      235      240
92 aag aag agg aag agg ggg tcc tga 744
93 Lys Lys Arg Lys Arg Gly Ser
94      245
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 247
99 <212> TYPE: PRT
100 <213> ORGANISM: Hordeum vulgare
102 <400> SEQUENCE: 2
103 Met Asp Ala Phe Tyr Ser Thr Ser Ser Ala Ala Ala Ser Gly Trp Gly
104 1      5      10      15
106 His Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val Gln Ser
107      20      25      30
109 His Leu Lys Leu Val Tyr Leu Thr Leu Cys Phe Ala Leu Ala Ser Ser
110      35      40      45
112 Ala Val Gly Ala Tyr Leu His Ile Ala Leu Asn Ile Gly Gly Met Leu
113      50      55      60
115 Thr Met Leu Ala Cys Val Gly Thr Ile Ala Trp Met Phe Ser Val Pro
116 65      70      75      80
118 Val Tyr Glu Glu Arg Lys Arg Phe Gly Leu Leu Met Gly Ala Ala Leu
119      85      90      95
121 Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Glu Leu Ala Ile Asp Phe
122      100      105      110
124 Asp Pro Ser Ile Leu Val Thr Gly Phe Val Gly Thr Ala Ile Ala Phe
125      115      120      125
127 Gly Cys Phe Ser Gly Ala Ala Ile Ile Ala Lys Arg Arg Glu Tyr Leu

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128      130      135      140
130 Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Ile Leu Leu Trp Leu
131 145      150      155      160
133 Gln Phe Val Thr Ser Ile Phe Gly His Ser Ser Gly Ser Phe Met Phe
134      165      170      175
136 Glu Val Tyr Phe Gly Leu Leu Ile Phe Leu Gly Tyr Met Val Tyr Asp
137      180      185      190
139 Thr Gln Glu Ile Ile Glu Arg Ala His His Gly Asp Met Asp Tyr Ile
140      195      200      205
142 Lys His Ala Leu Thr Leu Phe Thr Asp Phe Val Ala Val Leu Val Arg
143      210      215      220
145 Val Leu Ile Ile Met Leu Lys Asn Ala Gly Asp Lys Ser Glu Asp Lys
146 225      230      235      240
148 Lys Lys Arg Lys Arg Gly Ser
149      245
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 1067
154 <212> TYPE: DNA
155 <213> ORGANISM: Arabidopsis thaliana
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (1)..(741)
160 <223> OTHER INFORMATION: coding for BII-protein
162 <400> SEQUENCE: 3
163 atg gat gcg ttc tct tcc ttc ttc gat tct caa cct ggt agc aga agc 48
164 Met Asp Ala Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser
165 1 5 10 15
167 tgg agc tat gat tct ctt aaa aac ttc cgt cag att tct cca gcc gtt 96
168 Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val
169 20 25 30
171 cag aat cat ctt aaa cgg gtt tat ttg acc tta tgt tgt gct ctt gtg 144
172 Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
173 35 40 45
175 gcg tct gcc ttt gga gct tac ctc cat gtg ctc tgg aat atc ggc ggt 192
176 Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
177 50 55 60
179 att ctt aca acg att gga tgt att gga act atg att tgg ctc ctt tca 240
180 Ile Leu Thr Thr Ile Gly Cys Ile Gly Thr Met Ile Trp Leu Leu Ser
181 65 70 75 80
183 tgt cct cct tat gaa cac caa aaa agg ctt tct ctt ctg ttt gtg tct 288
184 Cys Pro Pro Tyr Glu His Gln Lys Arg Leu Ser Leu Leu Phe Val Ser
185 85 90 95
187 gct gtt ctt gaa ggt gct tct gtt ggc ccc ttg atc aaa gtg gca att 336
188 Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Ile
189 100 105 110
191 gat gtt gac cca agc atc ctt atc act gca ttt gtt gga act gcg ata 384
192 Asp Val Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
193 115 120 125
195 gcg ttt gtc tgt ttc tca gca gca gca atg tta gca aga cgc agg gag 432

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196 Ala Phe Val Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg Glu
197      130              135              140
199 tat ctc tac ctt gga gga ctg ctt tca tct ggc ttg tct atg cta atg 480
200 Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
201 145              150              155              160
203 tgg ctc cag ttt gcc tct tca atc ttt ggt ggc tct gca tct atc ttt 528
204 Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
205      165              170              175
207 aag ttt gag ttg tac ttt gga ctt ttg atc ttt gtg gga tac atg gtg 576
208 Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
209      180              185              190
211 gtg gac aca caa gag att ata gaa aag gca cac ctc ggt gac atg gac 624
212 Val Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
213      195              200              205
215 tat gta aaa cat tcg ttg acc ctt ttc act gac ttt gta gct gtg ttt 672
216 Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
217      210              215              220
219 gtt cgg att ctc atc ata atg ttg aag aac tca gca gat aaa gaa gag 720
220 Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
221 225              230              235              240
223 aag aag aag aaa agg aga aac tgaggggatg taaagtaa ttaactttat 771
224 Lys Lys Lys Lys Arg Arg Asn
225      245
227 ggttggttattc gtgtgtggcc actttgaaga tattacttgt tagcactctc tattggtgac 831
229 cagacatggtt tccactaaaa aggatctgct tggttcactt ctgcacaagt accatcttca 891
231 gattgtaaat gactcgagtg ttgttcttct tttcataaac ttttgttctt taagagtttg 951
233 gttctactga ttgcatctta ccaagctaag aataatgtag gaaaatgata atcctgttta 1011
235 aattttctaa aatgtgtgca tttcagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1067
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 247
240 <212> TYPE: PRT
241 <213> ORGANISM: Arabidopsis thaliana
243 <400> SEQUENCE: 4
244 Met Asp Ala Phe Ser Ser Phe Phe Asp Ser Gln Pro Gly Ser Arg Ser
245 1 5 10 15
247 Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro Ala Val
248 20 25 30
250 Gln Asn His Leu Lys Arg Val Tyr Leu Thr Leu Cys Cys Ala Leu Val
251 35 40 45
253 Ala Ser Ala Phe Gly Ala Tyr Leu His Val Leu Trp Asn Ile Gly Gly
254 50 55 60
256 Ile Leu Thr Thr Ile Gly Cys Ile Gly Thr Met Ile Trp Leu Leu Ser
257 65 70 75 80
259 Cys Pro Pro Tyr Glu His Gln Lys Arg Leu Ser Leu Leu Phe Val Ser
260 85 90 95
262 Ala Val Leu Glu Gly Ala Ser Val Gly Pro Leu Ile Lys Val Ala Ile
263 100 105 110
265 Asp Val Asp Pro Ser Ile Leu Ile Thr Ala Phe Val Gly Thr Ala Ile
266 115 120 125

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268 Ala Phe Val Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg Glu
269      130                      135                      140
271 Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Leu Ser Met Leu Met
272 145                      150                      155                      160
274 Trp Leu Gln Phe Ala Ser Ser Ile Phe Gly Gly Ser Ala Ser Ile Phe
275                      165                      170                      175
277 Lys Phe Glu Leu Tyr Phe Gly Leu Leu Ile Phe Val Gly Tyr Met Val
278                      180                      185                      190
280 Val Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met Asp
281                      195                      200                      205
283 Tyr Val Lys His Ser Leu Thr Leu Phe Thr Asp Phe Val Ala Val Phe
284      210                      215                      220
286 Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ser Ala Asp Lys Glu Glu
287 225                      230                      235                      240
289 Lys Lys Lys Lys Arg Arg Asn
290                      245
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 1160
295 <212> TYPE: DNA
296 <213> ORGANISM: Nicotiana tabacum
298 <220> FEATURE:
299 <221> NAME/KEY: CDS
300 <222> LOCATION: (1)..(747)
301 <223> OTHER INFORMATION: coding for BII-protein
303 <400> SEQUENCE: 5
304 atg gag tct tgc aca tcg ttc ttc aat tca cag tcg gcg tcg tct cgc      48
305 Met Glu Ser Cys Thr Ser Phe Phe Asn Ser Gln Ser Ala Ser Ser Arg
306      1                      5                      10                      15
308 aat cgc tgg agt tac gat tct ctt aag aac ttc cgc cag atc tct ccc      96
309 Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn Phe Arg Gln Ile Ser Pro
310                      20                      25                      30
312 ttt gtt caa act cat ctc aaa aag gtc tac ctt tca tta tgt tgt gct      144
313 Phe Val Gln Thr His Leu Lys Lys Val Tyr Leu Ser Leu Cys Cys Ala
314                      35                      40                      45
316 tta gtt gct tcg gct gct gga gct tac ctt cac att ctt tgg aac att      192
317 Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile
318      50                      55                      60
320 ggt ggc tta ctt acg aca ttg gga tgt gtg gga agc ata gtg tgg ctg      240
321 Gly Gly Leu Leu Thr Thr Leu Gly Cys Val Gly Ser Ile Val Trp Leu
322 65                      70                      75                      80
324 atg gcg aca cct ctg tat gaa gag caa aag agg ata gca ctt ctg atg      288
325 Met Ala Thr Pro Leu Tyr Glu Glu Gln Lys Arg Ile Ala Leu Leu Met
326                      85                      90                      95
328 gca gct gca ctg ttt aaa gga gca tct att ggt cca ctg att gaa ttg      336
329 Ala Ala Ala Leu Phe Lys Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu
330                      100                      105                      110
332 gct att gac ttt gac cca agc att gtg atc ggt gct ttt gtt ggt tgt      384
333 Ala Ile Asp Phe Asp Pro Ser Ile Val Ile Gly Ala Phe Val Gly Cys
334      115                      120                      125

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/548,748

DATE: 09/23/2005  
TIME: 14:52:54

Input Set : A:\Sequence listing - 12810-00137-US.txt  
Output Set: N:\CRF4\09232005\J548748.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 1046,1047,1048,1049,1050,1051,1052,1053,1054,1055,1056,1057  
Seq#:13; N Pos. 1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069  
Seq#:13; N Pos. 1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081  
Seq#:13; N Pos. 1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093  
Seq#:13; N Pos. 1094,1095  
Seq#:34; N Pos. 9590,9764  
Seq#:36; N Pos. 9590,9764  
Seq#:45; Xaa Pos. 4  
Seq#:46; Xaa Pos. 2,6  
Seq#:55; Xaa Pos. 4

## VERIFICATION SUMMARY

DATE: 09/23/2005

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Input Set : A:\Sequence listing - 12810-00137-US.txt

Output Set: N:\CRF4\09232005\J548748.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:997  
M:341 Repeated in SeqNo=13  
L:2034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:9540  
M:341 Repeated in SeqNo=34  
L:2379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:9540  
M:341 Repeated in SeqNo=36  
L:3092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0  
L:3117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0  
L:3328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0